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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=3; day=20; hr=16; min=3; sec=28; ms=753; ]

=====

\*\*\*\*\*

Reviewer Comments:

<150> US 60/430,654

<151> 2002 04 02

Please insert the current Application and date as <140>, and <141>, delete the non-ascii character in date line <151>.

<210> 1

<211> 34

<212> PRT

<213> T. CRUZI

<400> Sequence: 51

The above attached sequence appears after the sequence id 50, If it is a continuation please number is as 51 and change the Total number of sequences in <160> as 57.

\*\*\*\*\*

Application No: 10726692 Version No: 3.0

**Input Set:****Output Set:**

**Started:** 2008-02-29 21:19:36.478  
**Finished:** 2008-02-29 21:19:46.462  
**Elapsed:** 0 hr(s) 0 min(s) 9 sec(s) 984 ms  
**Total Warnings:** 57  
**Total Errors:** 257  
**No. of SeqIDs Defined:** 50  
**Actual SeqID Count:** 57

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <151>
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)

**Input Set:**

**Output Set:**

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**Total Errors:** 257

**No. of SeqIDs Defined:** 50

**Actual SeqID Count:** 57

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed
E 323	Invalid/missing amino acid numbering SEQID (33) POS (995)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1010)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1025)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1040)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1055)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1070)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1085)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1100)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1115)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1130)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1145)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1160)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1175)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1190)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1205)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1220)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1235)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1250)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1265)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1280) This error has occurred more than 20 times, will not be displayed

Input Set:

Output Set :

**Started:** 2008-02-29 21:19:36.478

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**Elapsed:** 0 hr(s) 0 min(s) 9 sec(s) 984 ms

Total Warnings: 57

Total Errors: 257

No. of SeqIDs Defined: 50

Actual SeqID Count: 57

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 212	Invalid Sequence ID Number; Expected 51 as next SeqID but skipped
E 202	Invalid input format; Value must be an integer in <400> SEQID: (1)

**Input Set:**

**Output Set:**

**Started:** 2008-02-29 21:19:36.478  
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**Total Warnings:** 57  
**Total Errors:** 257  
**No. of SeqIDs Defined:** 50  
**Actual SeqID Count:** 57

Error code	Error Description
E 202	Invalid input format; Value must be an integer in <400> SEQID: (2)
E 249	Order Sequence Error <210> -> <212>; Expected Mandatory Tag: <211> in SEQID ( 3 )
E 202	Invalid input format; Value must be an integer in <400> SEQID: (3)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (4)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (5)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (6)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (7)
E 252	Calc# of Seq. differs from actual; 50 seqIds defined; count=57
E 250	Structural Validation Error; Sequence listing may not be indexable

## SEQUENCE LISTING

<110> KIRCHHOFF, LOUIS V  
KEIKO, OTSU

<120> RECOMBINANT POLYPEPTIDES FOR DIAGNOSING INFECTION WITH  
TRYPANOSOMA CRUZI

<130> PNL21311A

<150> US 60/430,654

<151> 2002 04 02

<160> 50

<170> PatentIn version 3.2

<210> 1

<211> 1521

<212> DNA

<213> T. CRUZI

<220>

<221> CDS

<222> (1)..(1521)

<400> 1

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Tyr	Gly	Pro	Ser	Cys	Gly	Ala		Gly	Trp	Ser	Ala	Leu	Arg	Gly	Gly	
1				5					10					15		

caa	tgc	caa	caa	cct	cgt	tcg	aga	aat	ctc	caa	tgg	cgt	tgt	cac	ttc	96
Gln	Cys	Gln	Gln	Pro	Arg	Ser	Arg	Asn	Leu	Gln	Trp	Arg	Cys	His	Phe	
				20				25						30		

gtt	tat	tac	gga	agg	act	gct	ggg	ccc	atc	gta	cat	caa	acc	gta	cag	144
Val	Tyr	Tyr	Gly	Arg	Thr	Ala	Gly	Pro	Ile	Val	His	Gln	Thr	Val	Gln	
			35					40				45				

ccg	tac	aaa	tgg	cgc	tca	tga	ctt	gtt	tgt	gtc	gga	cac	ggg	caa	atc	192
Pro	Tyr	Lys	Trp	Arg	Ser		Leu	Val	Cys	Val	Gly	His	Gly	Gln	Ile	
		50					55					60				

acg	cat	cat	ttt	tgc	ccc	acc	tca	gaa	aaa	aac	gtt	cat	cac	agt	gtt	240
Thr	His	His	Phe	Cys	Pro	Thr	Ser	Glu	Lys	Asn	Val	His	His	Ser	Val	
		65					70				75					

tat	aac	agg	att	cca	gcc	gga	tgt	tct	tca	aat	tag	cga	gaa	gag	tcg	288
Tyr	Asn	Arg	Ile	Pro	Ala	Gly	Cys	Ser	Ser	Asn		Arg	Glu	Glu	Ser	
	80					85					90					

ttt	gat	gtt	tgc	cat	ctg	caa	ttc	cac	gaa	aat	tct	tgc	gat	taa	tat	336
Phe	Asp	Val	Cys	His	Leu	Gln	Phe	His	Glu	Asn	Ser	Cys	Asp		Tyr	
	95					100					105					

gca ggg agc cac aac ccc gaa gga gta ctg gca agt tgg aaa tgc gga	384
Ala Gly Ser His Asn Pro Glu Gly Val Leu Ala Ser Trp Lys Cys Gly	
110 115 120	
ctg cat ggg cta tca gag ttc cct cat gct cac gac cga gga gga taa	432
Leu His Gly Leu Ser Glu Phe Pro His Ala His Asp Arg Gly Gly	
125 130 135	
act cct cta cta cgg cat att aaa tgg aac ccc atc cat cat gtc ttt	480
Thr Pro Leu Leu Arg His Ile Lys Trp Asn Pro Ile His His Val Phe	
140 145 150 155	
acc cgc cac caa aac gaa gac gga agc acc cag aat ttg ccc gga tgt	528
Thr Arg His Gln Asn Glu Asp Gly Ser Thr Gln Asn Leu Pro Gly Cys	
160 165 170	
gtt gtt gca gtg gcc aca tgg gcc cat tgt ttc gct tgt gaa tat taa	576
Val Val Ala Val Ala Thr Trp Ala His Cys Phe Ala Cys Glu Tyr	
175 180 185	
caa aca tgc att tta cgt tgt tac cgc ctc caa tgt ata cat tgt aca	624
Gln Thr Cys Ile Leu Arg Cys Tyr Arg Leu Gln Cys Ile His Cys Thr	
190 195 200	
tga tgg ctc gta tca tcc gac tgg atc cat ggc cca gct cca aca ggc	672
Trp Leu Val Ser Ser Asp Trp Ile His Gly Pro Ala Pro Thr Gly	
205 210 215	
aga aaa taa tat cac taa ttc caa aaa aga aat gac aaa gct acg aga	720
Arg Lys Tyr His Phe Gln Lys Arg Asn Asp Lys Ala Thr Arg	
220 225 230	
aaa agt gaa aaa ggc cga gaa aga aaa att gga cgc cat taa ccg ggc	768
Lys Ser Glu Lys Gly Arg Glu Arg Lys Ile Gly Arg His Pro Gly	
235 240 245	
aac caa gct gga aga gga acg aaa cca agc gta caa agc agc aca caa	816
Asn Gln Ala Gly Arg Gly Thr Lys Pro Ser Val Gln Ser Ser Thr Gln	
250 255 260	
ggc aga gga gga aaa ggc taa aac att tca acg cct tat aac att tga	864
Gly Arg Gly Gly Lys Gly Asn Ile Ser Thr Pro Tyr Asn Ile	
265 270 275	
gtc gga aaa tat taa ctt aaa gaa aag gcc aaa tga cgc agt ttc aaa	912
Val Gly Lys Tyr Leu Lys Glu Lys Ala Lys Arg Ser Phe Lys	
280 285 290	
tcg gga taa gaa aaa aaa ttc tga aac cgc aaa aac tga cga agt aga	960
Ser Gly Glu Lys Lys Phe Asn Arg Lys Asn Arg Ser Arg	
295 300	
gaa aca gag ggc ggc tga ggc tgc caa ggc cgt gga gac gga gaa gca	1008
Glu Thr Glu Gly Gly Gly Cys Gln Gly Arg Gly Asp Gly Glu Ala	
305 310 315	

gag ggc agc tga ggc cac gaa ggt tgc cga agc gga gaa gcg gaa ggc	1056
Glu Gly Ser Gly His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly	
320 325 330	
agc tga ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc agc tga	1104
Ser Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser	
335 340 345	
agc cac gaa ggt tgc cga agc gga gaa gca gaa ggc agc tga ggc cgc	1152
Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser Gly Arg	
350 355 360	
caa ggc cgt gga gac gga gaa gca gag ggc agc tga agc cac gaa ggt	1200
Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser Ser His Glu Gly	
365 370 375	
tgc cga agc gga gaa gca gag ggc agc tga agc cat gaa ggt tgc cga	1248
Cys Arg Ser Gly Glu Ala Glu Gly Ser Ser His Glu Gly Cys Arg	
380 385 390	
agc gga gaa gca gaa ggc agc tga ggc cgc caa ggc cgt gga gac gga	1296
Ser Gly Glu Ala Glu Gly Ser Gly Arg Gln Gly Arg Gly Asp Gly	
395 400 405	
gaa gca gag ggc agc tga agc cac gaa ggt tgc cga agc gga gaa gca	1344
Glu Ala Glu Gly Ser Ser His Glu Gly Cys Arg Ser Gly Glu Ala	
410 415 420	
gaa ggc agc tga ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc	1392
Glu Gly Ser Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly	
425 430 435	
agc tga agc cac gaa ggt tgc cga agc gga gaa gca gaa ggc agc tga	1440
Ser Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser	
440 445 450	
ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc agc tga agc cac	1488
Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser Ser His	
455 460 465	
gaa ggt tgc cga agc gga gaa gga tat cga tcc	1521
Glu Gly Cys Arg Ser Gly Glu Gly Tyr Arg Ser	
470 475	

<210> 2

<211> 7

<212> PRT

<213> T. CRUZI

<400> 2

Tyr Gly Pro Ser Cys Gly Ala  
1 5



<210> 3  
<211> 46  
<212> PRT  
<213> T. CRUZI

<400> 3

Gly Trp Ser Ala Leu Arg Gly Gly Gln Cys Gln Gln Pro Arg Ser Arg  
1 5 10 15

Asn Leu Gln Trp Arg Cys His Phe Val Tyr Tyr Gly Arg Thr Ala Gly  
20 25 30

Pro Ile Val His Gln Thr Val Gln Pro Tyr Lys Trp Arg Ser  
35 40 45

<210> 4  
<211> 36  
<212> PRT  
<213> T. CRUZI

<400> 4

Leu Val Cys Val Gly His Gly Gln Ile Thr His His Phe Cys Pro Thr  
1 5 10 15

Ser Glu Lys Asn Val His His Ser Val Tyr Asn Arg Ile Pro Ala Gly  
20 25 30

Cys Ser Ser Asn  
35

<210> 5  
<211> 18  
<212> PRT  
<213> T. CRUZI

<400> 5

Arg Glu Glu Ser Phe Asp Val Cys His Leu Gln Phe His Glu Asn Ser  
1 5 10 15

Cys Asp

<210> 6  
<211> 32  
<212> PRT

<213> T. CRUZI

<400> 6

Tyr Ala Gly Ser His Asn Pro Glu Gly Val Leu Ala Ser Trp Lys Cys  
1 5 10 15

Gly Leu His Gly Leu Ser Glu Phe Pro His Ala His Asp Arg Gly Gly  
20 25 30

<210> 7

<211> 47

<212> PRT

<213> T. CRUZI

<400> 7

Thr Pro Leu Leu Arg His Ile Lys Trp Asn Pro Ile His His Val Phe  
1 5 10 15

Thr Arg His Gln Asn Glu Asp Gly Ser Thr Gln Asn Leu Pro Gly Cys  
20 25 30

Val Val Ala Val Ala Thr Trp Ala His Cys Phe Ala Cys Glu Tyr  
35 40 45

<210> 8

<211> 16

<212> PRT

<213> T. CRUZI

<400> 8

Gln Thr Cys Ile Leu Arg Cys Tyr Arg Leu Gln Cys Ile His Cys Thr  
1 5 10 15

<210> 9

<211> 17

<212> PRT

<213> T. CRUZI

<400> 9

Trp Leu Val Ser Ser Asp Trp Ile His Gly Pro Ala Pro Thr Gly Arg  
1 5 10 15

Lys

<210> 10  
<211> 23  
<212> PRT  
<213> T. CRUZI

<400> 10

Phe Gln Lys Arg Asn Asp Lys Ala Thr Arg Lys Ser Glu Lys Gly Arg  
1 5 10 15

Glu Arg Lys Ile Gly Arg His  
20

<210> 11  
<211> 24  
<212> PRT  
<213> T. CRUZI

<400> 11

Pro Gly Asn Gln Ala Gly Arg Gly Thr Lys Pro Ser Val Gln Ser Ser  
1 5 10 15

Thr Gln Gly Arg Gly Gly Lys Gly  
20

<210> 12  
<211> 8  
<212> PRT  
<213> T. CRUZI

<400> 12

Asn Ile Ser Thr Pro Tyr Asn Ile  
1 5

<210> 13  
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<212> PRT  
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<400> 13

Val Gly Lys Tyr  
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<210> 14  
<211> 6  
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<213> T. CRUZI

<400> 14

Leu Lys Glu Lys Ala Lys  
1 5

<210> 15

<211> 6

<212> PRT

<213> T. CRUZI

<400> 15

Arg Ser Phe Lys Ser Gly  
1 5

<210> 16

<211> 4

<212> PRT

<213> T. CRUZI

<400> 16

Glu Lys Lys Phe  
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<210> 17

<211> 4

<212> PRT

<213> T. CRUZI

<400> 17

Asn Arg Lys Asn  
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<210> 18

<211> 8

<212> PRT

<213> T. CRUZI

<400> 18

Arg Ser Arg Glu Thr Glu Gly Gly  
1 5

<210> 19

<211> 13

<212> PRT

<213> T. CRUZI

<400> 19

Gly Cys Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 20

<211> 13

<212> PRT

<213> T. CRUZI

<400> 20

Gly His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 21

<211> 13

<212> PRT

<213> T. CRUZI

<400> 21

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 22

<211> 13

<212> PRT

<213> T. CRUZI

<400> 22

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 23

<211> 13

<212> PRT

<213> T. CRUZI

<400> 23

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 24

<211> 13

<212> PRT

<213> T. CRUZI

<400> 24

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 25

<211> 13

<212> PRT

<213> T. CRUZI

<400> 25

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 26

<211> 13

<212> PRT

<213> T. CRUZI

<400> 26

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 27

<211> 13

<212> PRT

<213> T. CRUZI

<400> 27

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 28

<211> 13

<212> PRT

<213> T. CRUZI

<400> 28

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 29

<211> 13

<212> PRT

<213> T. CRUZI

<400> 29

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 30

<211> 13

<212> PRT

<213> T. CRUZI

<400> 30

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 31

<211> 13

<212> PRT

<213> T. CRUZI

<400> 31

Ser His Glu Gly Cys Arg Ser Gly Glu Gly Tyr Arg Ser  
1 5 10

<210> 32

<211> 42

<212> DNA

<213> T CRUZI

<220>

<221> misc\_feature

<222> (1)..(4)

<223> n is a, c, g, or t

<400> 32

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42

<210> 33

<211> 3749

<212> DNA

<213> T CRUZI

<220>

<221> CDS

<222> (833)..(2575)

<220>

<221> sig\_peptide

<222> (833)..(937)

<220>  
 <221> mat\_peptide  
 <222> (938)..(2575)

<400> 33

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cggtcaaaaag gatgtatata tacatatata accataaggg aaacatttgg gcatttaact	120
gcctttacat ttcccttttc cttcaatata ttgtttgttt gtttttggtt tctataggaa	180
attttaggat ccggccagcg gcataggaga ttattctctt ttttattaat tgcttaatgc	240
gttgggtctgt gtgtgtgttg gttcccttgt gcgagctcac ggggcctaata tatgattggt	300
gcgcataatgc atatatatat atatatatat acatgtgtgt gtgtgtgtat atgtacgttt	360
gttgggtttgc cgtgtactc ccgcctgcgt gtgtctgtct ctctctctgt gtgtgtgatg	420
ggctgcttct ctttcttttg ttgcgtccct ttattattat tttttttttt tcttctctcc	480
cacttctctc cccgtgtggt gcacgcacag taaagataga gggagaaata gagcgagtgt	540
ttgtatcagt gtctccgttg cggtcgttac tggtagaagg agaagaatag aagaaggaga	600
aaaaaaaaaa aaaaaaaaaa aaaagagaga gagagagaga agggcgaacg agaaaaaaga	660
agaagaaaca tttgagaagg aattggaacg aaaattgtaa gaggaagcaa aaaaaaaaaa	720
aaaaagtgtg tgtgtgtgag agagagagag agaggaagcc aataataata aaaagcaaac	780
aaaaaagcaa aaacaaaaat atttgtagac cggacgtccc gtcttggacg tg atg ttt	838
	Met Phe
	35
tca aaa agg acg tcg cca gca ccc ttc cgt gcg ctc ctg ctg ccg gtc	886
Ser Lys Arg Thr Ser Pro Ala Pro Phe Arg Ala Leu Leu Leu Pro Val	
30 25 20	
gtg gtg gtg gtg gtg gtg gtg gca tct gtg gcc ctc cct gca gga	934
Val Val Val Val Val Val Val Val Ala Ser Val Ala Leu Pro Ala Gly	
15 10 5	
gcg cag ttt gat tta agg cag cag cag ctg gtt ata cag gat ttc ttc	982
Ala Gln Phe Asp Leu Arg Gln Gln Gln Leu Val Ile Gln Asp Phe Phe	
1 1 5 10 15	
atc agt cgc tcc tgc gca gga tgt tca cag ggg caa acc gat ggc cca	1030
Ile Ser Arg Ser Cys Ala Gly Cys Ser Gln Gly Gln Thr Asp Gly Pro	
20 25 30	
agc ggt gcc ggc aca ctc ttc act gcc gcc ggt ggt tcg ctt ggc aaa	1078
Ser Gly Ala Gly Thr Leu Phe Thr Ala Ala Gly Gly Ser Leu Gly Lys	
35 40 45	
gat gct tcc acg ctg ctg ttg tgt gac caa ggt ggt ggt ggc tcc agc	1126



Asp	Ala	Ser	Thr	Leu	Leu	Leu	Cys	Asp	Gln	Gly	Gly	Gly	Gly	Ser	Ser	
		50					55					60				
gtg	cgt	ttg	gtg	aac	aaa	tcc	ggc	att	ttc	acc	ctt	gcc	ggt	agt	aaa	1174
Val	Arg	Leu	Val	Asn	Lys	Ser	Gly	Ile	Phe	Thr	Leu	Ala	Gly	Ser	Lys	
		65				70					75					
acg	acg	cgt	ggc	aat	caa	aat	ggg	ccg	gcg	gcg	acg	gca	ctc	ttc	aac	1222
Thr	Thr	Arg	Gly	Asn	Gln	Asn	Gly	Pro	Ala	Ala	Thr	Ala	Leu	Phe	Asn	
80					85					90					95	
atg	ccc	cga	gct	gtg	gtg	ctt	gag	gat	gga	gcg	ctt	tac	gtg	gcg	gac	1270
Met	Pro	Arg	Ala	Val	Val	Leu	Glu	Asp	Gly	Ala	Leu	Tyr	Val	Ala	Asp	
				100					105					110		
agt	gcc	aac	aac	ctc	gtt	cga	gaa	atc	tcc	aat	ggc	att	gtc	act	tcg	1318
Ser	Ala	Asn	Asn	Leu	Val	Arg	Glu	Ile	Ser	Asn	Gly	Ile	Val	Thr	Ser	
			115					120					125			
ttt	att	acg	gag	gga	ctg	ctg	ggc	cca	tcg	tac	atc	aaa	ccg	tac	agc	1366
Phe	Ile	Thr	Glu	Gly	Leu	Leu	Gly	Pro	Ser	Tyr	Ile	Lys	Pro	Tyr	Ser	
		130					135					140				
cgt	cca	aat	ggc	gcc	cat	gac	ttg	ttt	gtg	tcg	gac	acg	ggc	aaa	tct	1414
Arg	Pro	Asn	Gly	Ala	His	Asp	Leu	Phe	Val	Ser	Asp	Thr	Gly	Lys	Ser	
		145				150					155					
cgc	atc	att	ttt	gcc	cca	ctt	cag	aaa	caa	acg	ttc	atc	aca	gtg	ttt	1462
Arg	Ile	Ile	Phe	Ala	Pro	Leu	Gln	Lys	Gln	Thr	Phe	Ile	Thr	Val	Phe	
160					165					170					175	
ata	aca	gga	ttc	cag	ccg	gat	gtt	ctt	caa	att	agc	gag	aag	agt	cgt	1510
Ile	Thr	Gly	Phe	Gln	Pro	Asp	Val	Leu	Gln	Ile	Ser	Glu	Lys	Ser	Arg	
				180					185							